

10/528344

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> EXPRESSION SYSTEMS OF TOXIC PROTEINS, VECTORS
AND PROCESS FOR MANUFACTURING TOXIC PROTEINS

<130> B14143 EE

<140>

<141>

<150> FR N°02 11676

<151> 2002-09-20

<160> 53

<170> PatentIn Ver. 2.1

<210> 1

<211> 37

<212> PRT

<213> Hepatitis C virus

<400> 1

Met Ile Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe
1 5 10 15

Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu Leu Phe
20 25 30

Ala Gly Val Asp Ala
35

<210> 2

<211> 31

<212> PRT

<213> Hepatitis C virus

<400> 2

Met Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val
1 5 10 15

Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala
20 25 30

<210> 3

<211> 111

<212> DNA

<213> Hepatitis C virus

<400> 3

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aactgggcta aagttctggt tgttctgctg ctgttcgctg gtgttgacgc t 111

<210> 4

<211> 93

<212> DNA

<213> Hepatitis C virus

<400> 4

atggaatagc ttgttctgct gttcctgctg ctggctgacg ctcgtgtttg ctcttgccctg 60
tggatgatgc tgctgatctc tcaggctgaa gct 93

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (+) of insertion into pT7-7

<400> 5
 gggaatgccataatgatcgct ggtg 24

<210> 6
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (-) of insertion into pT7-7

<400> 6
 gcatatcgat ctaagcgatca aca 23

<210> 7
 <211> 131
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: TME1 coding sens DNA
 + 3' cla I site

<400> 7
 atgccatatg atcgctggtg ctactgggg tgttctggct ggtatcgctt acttctctat 60
 ggttggtaac tgggctaaag ttctggttgt tctgctgctg ttcgctgggtg ttgacgctta 120
 gatcgatatg c 131

<210> 8
 <211> 131
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: anticodant sens DNA
 + 5' cla I site

<400> 8
 gcatatcgat ctaagcgatca acaccagcga acagcagcag aacaaccaga actttagccc 60
 agttaccaac catagagaag taagcgatac cagccagaac accccagtga gcaccagcga 120
 tcatatggca t 131

<210> 9
 <211> 74
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 coding sens oligonucleotide for the synthesis of
 TME1

<400> 9
 atgccatatg atcgctggtg ctactgggg tgttctggct ggtatcgctt acttctctat 60

ggttggtaac tggg

74

<210> 10

<211> 79

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
anticoding sens oligonucleotide for the synthesis of
TME1

<400> 10

gcatatcgat ctaagcgtca acaccagcga acagcagcag aacaaccaga actttagccc 60
agttaccaac catagagaa 79

<210> 11

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pGEXKT without
the dp site

<400> 11

ggatccatgg aatacgttgt tc

22

<210> 12

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pGEXKT with
the dp site

<400> 12

ggatccgacc cgatggaata cgttgttc

28

<210> 13

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide (-) of insertion into pGEXKT

<400> 13

gaattcctaa gcttcagcct gag

23

<210> 14

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide (+) of transfert onto pET32a

<400> 14
 gtgatatctg atctgtctgg tgggtgg 27

<210> 15
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (+) of insertion into pT7-7

<400> 15
 cgcatatgga cccgatcgct ggtgct 26

<210> 16
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (-) of insertion into pT7-7

<400> 16
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<210> 17
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (+) of insertion into pT7-7

<400> 17
 catatggaat acgttggtc 19

<210> 18
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (-) of insertion into pT7-7

<400> 18
 aagcttaagc ttcagcctga gagatcag 28

<210> 19
 <211> 103
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: sens DNA
 coding TME2 + 5' Nde I site and 3' Hind III site

<400> 19
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 ctgtggatga tgctgctgat ctctcaggct gaagcttaag ctt 103

<210> 20
 <211> 103
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: sens DNA
 anticoding TME2 + 3' Nde I site and 5' Hind III site

<400> 20
 aagcttaagc ttcagcctga gagatcagca gcatcatcca caggcaagag caaacacgag 60
 cgtcagccag cagcaggaac agcagaacaa cgtattccat atg 103

<210> 21
 <211> 68
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 sens oligonucleotide (+) coding for the synthesis
 of TME2

<400> 21
 catatggaat acgttgttct gctgttcctg ctgctggctg acgctcgtgt ttgctcttgc 60
 ctgtggat 68

<210> 22
 <211> 57
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 sens oligonucleotide (-) coding for the synthesis
 of TME2

<400> 22
 aagcttaagc ttcagcctga gagatcagca gcatcatcca caggcaagac gaaacac 57

<210> 23
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (+) of insertion into pGEXKT without
 the dp site

<400> 23
 ggatccgaat acgttgttc 19

<210> 24
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (+) of insertion into pGEXKT with
 the dp site

<400> 24
ggatccgacc cggaatacgt tgttc 25

<210> 25
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (-) of insertion into pGEXKT with
the dp site

<400> 25
gaattcttaa gcttcagcct gagagatcag 30

<210> 26
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pT7-7

<400> 26
cgcatatgga cccggaatac gttgttc 27

<210> 27
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (-) of insertion into pT7-7

<400> 27
cagaattcct aagcttcagc ctgagag 27

<210> 28
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: end of the
GST followed by the thrombine site

<400> 28
Ser Asp Leu Ser Gly Gly Gly Gly Gly Leu Val Pro Arg Gly Ser
1 5 10 15

<210> 29
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: DNA
coding for GST protein in the pGEXKT vector

B141431-PCT.txt

<400> 29

atgtccccta	tactaggtta	ttggaaaatt	aagggccttg	tgcaaccac	tcgacttctt	60
ttggaatata	ttgaagaaaa	atatgaagag	catttgatg	agcgcatga	aggtgataaa	120
tggcgaaaca	aaaagtttga	attgggtttg	gagtttccca	atcttcctta	ttatattgat	180
ggtgatgtta	aattaacaca	gtctatggcc	atcatagctt	atatactga	caagcacaac	240
atgttgggtg	gttggtccaaa	agagcgtgca	gagatttcaa	tgcttgaagg	agcggttttg	300
gatattagat	acggtgtttc	gagaattgca	tatagtaaag	actttgaaac	tctcaaagtt	360
gattttctta	gcaagctacc	tgaaatgctg	aaaatgttcg	aagatcgttt	atgtcataaa	420
acatatattaa	atggtgatca	tgtaacccat	cctgacttca	tggtgatga	cgctcttgat	480
gttgttttat	acatggaccc	aatgtgcctg	gatgctgtcc	caaaattagt	ttgttttaaa	540
aaacgtattg	aagctatccc	acaaattgat	aagtacttga	aatccagcaa	gtatatagca	600
tggcctttgc	agggctggca	agccacgttt	gggtgggtg	accatcctcc	aaaatcggt	660
ctgtctggtg	gtggtggtgg	tctggttccg	cgtggatccc	cggaattca	tcgtgac	717

<210> 30

<211> 327

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: DNA
coding for the thioredoxine in the pET32a+ vector

<400> 30

atgagcgata	aaattattca	cctgactgac	gacagttttg	acacggatgt	actcaaagcg	60
gacggggcga	tcctcgtcga	tttctgggca	gagtgggtcg	gtccgtgcaa	aatgatcgcc	120
ccgattctgg	atgaaatcgc	tgacgaatat	cagggcaaac	tgaccgttgc	aaaactgaac	180
atcgatcaaa	accctggcac	tgcccgaaa	tatggcatcc	gtggtatccc	gactctgctg	240
ctgttcaaaa	acggtgaagt	ggcggcaacc	aaagtgggtg	cactgtctaa	aggtcagttg	300
aaagagttcc	tcgacgctaa	cctggcc				327

<210> 31

<211> 4969

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmide
expressing pGEXKT

<400> 31

acgttatcga	ctgcacggtg	caccaatgct	tctggcgctca	ggcagccatc	ggaagctgtg	60
gtatggctgt	gcaggctcgt	aatcactgca	taattcgtgt	cgctcaaggc	gcactcccgt	120
tctggataat	gttttttgcg	ccgacatcat	aacggttctg	gcaaattatc	tgaaatgagc	180
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cacaggaaac	agtattcatg	tcccctatac	taggttattg	gaaaattaa	ggccttgtgc	300
aaccactcgc	acttcttttg	gaatatcttg	aagaaaaata	tgaaagagcat	ttgtatgagc	360
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aattagtttg	ttttaaaaaa	cgtattgaa	ctatcccaca	aattgataag	tacttgaat	840
ccagcaagta	tatagcatgg	cttttgcagg	gctggcaagc	cacgtttggt	ggtggcgacc	900
atcctccaaa	atcggtatcg	tctggtgggt	gtggtgggtc	ggttccgcgt	ggatccccgg	960
gaattcatcg	tgactgactg	acgatctgcc	tcgcgcgttt	cggtgatgac	ggtgaaaacc	1020
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<210> 32

<211> 11800

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmide expressing pET32a+

<400> 32

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gaaccggcca	ggtagcgtc	gaggaactct	ttcaactgac	cttggcgcac	cgtggctctg	720
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ttttgcacgg	accgcaccac	caaaactagc	tacaagtcac	aacgttgcca	gtcaaacggg	1140
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<210> 34

<211> 813

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system
coding for fusion protein GST-DP-TME1

<400> 34

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ggtagtggtt aattaacaca gtctatggcc atcatacgtt atatactga caagcacaac 240
atgttgggtg gttgtccaaa agagcgtgca gagatttcaa tgcttgaagg agcggttttg 300
gatattagat acggtgtttc gagaattgca tatagtaaag actttgaaac tctcaaagt 360
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B141431-PCT.txt

```

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tggggtgttc tggctgggtat cgcttacttc tctatgggtg gtaactgggc taaagttctg 780
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```

<210> 35
 <211> 513
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: expression system
 coding for fusion protein TrX-DP-TME1

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<400> 35
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```

<210> 36
 <211> 117
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: expression system
 coding for fusion protein M-DP-TME1

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<400> 36
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gttgtaact gggctaaagt tctggtgtt ctgctgctgt tcgctgggtg tgacgct 117

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<210> 37
 <211> 795
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: expression system
 coding for fusion protein
 GST-DP-TME2

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<400> 37
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795

<210> 38
 <211> 486
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: expression system
 coding for fusion protein
 TrX-DP-TME2

<400> 38
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 gcttag 486

<210> 39
 <211> 99
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: expression system
 coding for fusion protein M-DP-TME2

<400> 39
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<210> 40
 <211> 5082
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: expression vector
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B141431-PCT.txt

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<210> 41
 <211> 5064
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: expression vector
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<213> Artificial sequence

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gactccccgt	cgtgtagata	actacgatac	gggagggtct	accatctggc	cccagtgcgt	4560
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ccggaagggc	cgagcgcaga	agtggtcctg	caactttatc	cgcttccatc	cagtctatta	4680
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tggcgagaaa	ggaaggggag	aaagcgaaag	gagcgggctg	tagggcgctg	gcaagtgtag	5820
cggtcacgct	gcgcgtaacc	accacacccg	ccgcgcttaa	tgcgccgcta	cagggcgctg	5880
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<210> 44

<211> 2617

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector
pT7-7-dp-Pt(TME1)

<400> 44

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actttagccc	agttaccaac	catagagaag	taagcgatac	cagccagaac	accccagtga	180
gcaccagcga	tcgggtccat	atgtatatct	ccttcttaaa	gttaaacaac	attatttcta	240
gagggaacc	gttggtgtct	ccctatagtg	agtcgtatta	atttcgaagt	ctatcagaag	300
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ctccgggaga	cggtcacagc	ttgtctgtaa	gcggatgccg	ggagcagaca	agcccgtcag	420
ggcgcgtcag	cgggtgttgg	cgggtgtcgg	ggcgcagcca	tgacccagtc	acgtagcgat	480
agcggagtgt	atatactggc	ttaactatgc	ggcatcagag	cagattgtac	tgagagtgc	540
ccataggaag	atcttccgga	agatcttcct	atgcgggtgtg	aaataaccgca	cagatgcgta	600
aggagaaaat	accgcacatc	gcgctcttcc	gcttctctgc	tcactgactc	gctgcgctgc	660

B141431-PCT.txt

gtcgttcggc	tgccggcagc	ggtatcagct	cactcaaagg	cggtaatagc	gttatccaca	720
gaatcagggg	ataacgcagg	aaagaacatg	tgagcaaaa	gccagcaaaa	ggccaggaac	780
cgtaaaaagg	ccgcgtttgc	ggcgtttttc	cataggctcc	gccccctga	cgagcatcac	840
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ctcagttcgg	tgtaggtcgt	tcgctccaag	ctgggctgtg	tgcacgaacc	ccccgttcag	1080
cccagccgct	gcgccttatc	cggtaaactat	cgtcttgagt	ccaaccgggt	aagacacgac	1140
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gctacagagt	tcttgaagtg	gtggcctaac	tacggctaca	ctagaaggac	agtatttggt	1260
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tcggtcgccg	catacactat	tctcagaatg	acttggttga	gtactacca	gtcacagaaa	2040
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ataacactgc	ggccaactta	cttctgacaa	cgatcggagg	accgaaggag	ctaaccgctt	2160
ttttgcacaa	catgggggat	catgtaactc	gccttgatcg	ttgggaaccg	gagctgaatg	2220
aagcataacc	aaacgacgag	cgtgacacca	cgtagcctgt	agcaatggca	acaacgttgc	2280
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cagatggtaa	gccctcccgt	atcgtagtta	tctacacgac	ggggagtcag	gcaactatgg	2520
atgaacgaaa	tagacagatc	gctgagatag	gtgcctcact	gattaagcat	tggtaaactgt	2580
cagaccaagt	ttactcatat	atactttaga	ttgatttt			2617

<210> 45

<211> 2599

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector
pT7-7-dp-Pt(TME2)

<400> 45

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caagagcaaa	cacgagcgtc	agccagcagc	aggaacagca	gaacaacgta	ttccgggtcc	180
atatgtatat	ctccttctta	aagttaaaca	aaattatttc	tagagggaaa	ccgttggtgt	240
ctccctatat	tgagtcgtag	taatttcgaa	gtctatcaga	agttcgaatc	gctgggcctc	300
gcgcgtttcg	gtgatgacgg	tgaaaacctc	tgacacatgc	agctcccgga	gacggtcaca	360
gcttgctctg	aagcggatgc	cgggagcaga	caagcccgtc	agggcgcgct	agcgggtgtt	420
ggcgggtgtc	ggggcgcagc	catgaccag	tcacgtagcg	atagcggagt	gtatatactg	480
gcttaactat	gcggcatcag	agcagattgt	actgagagtg	caccatagga	agatcttccg	540
gaagatcttc	ctatgcgggtg	tgaaataccg	cacagatgcg	taaggagaaa	ataccgcata	600
aggcgctctt	ccgcttcttc	gtcactgac	tcgctgcgct	cggtcggttc	gctgcggcga	660
gcggtatcag	ctcactcaaa	ggcggtaata	cggttatcca	cagaatcagg	ggataacgca	720
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gccactggta	acaggattag	cagagcgagg	tatgtaggcg	gtgctacaga	gttcttgaag	1200
tgggtggccta	actacggcta	cactagaagg	acagtatttg	gtatctgcgc	tctgctgaag	1260
ccagttacct	tcggaaaaag	agttggtagc	tcttgatccg	gcaaaaaaac	caccgctgggt	1320
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B141431-PCT.txt

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<210> 46

<211> 271

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: fusion protein
GST-DP-TME1

<400> 46

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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
          20          25          30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
          35          40          45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
          50          55          60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
          65          70          75          80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
          85          90          95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
          100          105          110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
          115          120          125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
          130          135          140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
          145          150          155          160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
          165          170          175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
          180          185          190

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B141431-PCT.txt

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
210 215 220
Gly Gly Gly Leu Val Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His
225 230 235 240
Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp
245 250 255
Ala Lys Val Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
260 265 270

<210> 47
<211> 265
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
GST-DP-TME2

<400> 47
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
210 215 220

B141431-PCT.txt

Gly Gly Gly Leu Val Pro Arg Gly Ser Asp Pro Glu Tyr Val Val Leu
 225 230 235 240
 Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys Ser Cys Leu Trp Met
 245 250 255
 Met Leu Leu Ile Ser Gln Ala Glu Ala
 260 265

<210> 48
 <211> 170
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: fusion protein
 TrX-DP-TME1

<400> 48
 Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
 1 5 10 15
 Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
 20 25 30
 Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
 35 40 45
 Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
 50 55 60
 Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
 65 70 75 80
 Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
 85 90 95
 Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
 100 105 110
 Ser Gly Ser Pro Lys Ser Asp Leu Ser Gly Gly Gly Gly Gly Leu Val
 115 120 125
 Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala
 130 135 140
 Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val
 145 150 155 160
 Val Leu Leu Leu Phe Ala Gly Val Asp Ala
 165 170

<210> 49
 <211> 161
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: fusion protein
 TrX-DP-TME2

<400> 49
 Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
 1 5 10 15

Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
 20 25 30
 Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
 35 40 45
 Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
 50 55 60
 Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
 65 70 75 80
 Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
 85 90 95
 Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
 100 105 110
 Ser Gly Ser Asp Leu Ser Gly Gly Gly Gly Leu Val Pro Arg Gly
 115 120 125
 Ser Asp Pro Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala
 130 135 140
 Arg Val Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu
 145 150 155 160
 Ala

<210> 50
 <211> 39
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: fusion protein
 M-DP-TME1

<400> 50
 Met Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala
 1 5 10 15
 Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu
 20 25 30
 Leu Phe Ala Gly Val Asp Ala
 35

<210> 51
 <211> 33
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: fusion protein
 M-DP-TME2

<400> 51
 Met Asp Pro Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala
 1 5 10 15
 Arg Val Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu
 20 25 30
 Ala

<210> 52
 <211> 239
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 glutathion transferase (GST)

<400> 52
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
 210 215 220
 Gly Gly Gly Leu Val Pro Arg Gly Ser Pro Gly Ile His Arg Asp
 225 230 235

<210> 53
 <211> 170
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 thioredoxine (TrX)

<400> 53

Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
 1 5 10 15
 Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
 20 25 30
 Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
 35 40 45
 Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
 50 55 60
 Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
 65 70 75 80
 Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
 85 90 95
 Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
 100 105 110
 Ser Gly Ser Pro Lys Ser Asp Leu Ser Gly Gly Gly Gly Gly Leu Val
 115 120 125
 Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala
 130 135 140
 Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val
 145 150 155 160
 Val Leu Leu Leu Phe Ala Gly Val Asp Ala
 165 170